



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/359,026
Art Unit / Team No.: 1649
Date Processed by STIC: 12/15/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/359,026

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/359,026

DATE: 12/15/1999
TIME: 10:39:47

Input Set: I359026.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: TOBIN PHD, ELAINE
2 SUGANO PHD, SHOJI
3 <120> TITLE OF INVENTION: REGULATION OF CIRCADIAN RHYTHMS
4 <130> FILE REFERENCE: 36316.7
5 <140> CURRENT APPLICATION NUMBER: US/09/359,026
6 <141> CURRENT FILING DATE: 1999-07-22
7 <160> NUMBER OF SEQ ID NOS: 2
8 <170> SOFTWARE: PatentIn Ver. 2.0
9 <210> SEQ ID NO 1
10 <211> LENGTH: 1097
11 <212> TYPE: DNA
12 <213> ORGANISM: Arabidopsis thaliana
13 <400> SEQUENCE: 1
14 gtcgaccac gcgccgaga agaaaaccct agatttctcc gtctctctaa tttcctttct 60
15 ctctcaagct tctcagaaag tctgacactt tcgagaatct aatctccaaa tttcttgtct 120
16 ttttgagaa ggaatcgaat tatgtacaag gaacgtatgt gaggaggtgg tgggtgggtca 180
17 tcgagatcag agatcctcgg tggagctatt gatcggaac gaatcaacga tgcactcaat 240
18 aagaaactag agaaatcttc aacttccacc accacatcta gggttttctc ttctaaagac 300
19 aaagatccct tttccttcac atctactaaa actcagcttc ctgatgtgga atcggaact 360
20 gatagtgaag ggtctgatgt gagtggatcg gagggtgatg atacgtcgtg gatctcttgg 420
21 ttttgtaatt tgagagggaa tgatttcttc tgtgaagtcg atgaagatta tattcaagat 480
22 gatttcaatc tttgtggttt aagtggtaaa gtcccttact atgattatgc acttgatctc 540
23 atttttagatg ttgatgcttc caacagttag atgtttactg atgaacagca tgaaatgggtg 600
24 gaatcagctg ctgagatgct atatggtctt attcatgttc gttacatttt gactactaaa 660
25 ggaatggctg caatgactga gaagtacaag aactgtgatt tcgggagatg cccgagagtt 720
26 ttctgttgcg gtcagtcttg tcttccagtt ggacaatccg atatcccag atcgagtact 780
27 gtgaagatat actgccctaa atgcgaggat atatcttacc cgcgatctaa attccaaggc 840
28 aatattgatg gagcgtactt tggaaccaca ttcctcact tgttcttgat gacttacggg 900
29 aacttaaagc cgcagaagcc tactcaaagc tatgtcccaa aaatctttgg cttcaaggta 960
30 cacaaccat gatactagtg ctctgcattc tcaatggatg tacatttagt ggctctgtaa 1020
31 ttgcatccgg atgagcaact gaaacgatag ctgcggtgac tggagcatac atcaaccatt 1080
32 cwndwsdskt sttcstt 1097
W-->
33 <210> SEQ ID NO 2
34 <211> LENGTH: 276
35 <212> TYPE: PRT
36 <213> ORGANISM: Arabidopsis thaliana
37 <400> SEQUENCE: 2
38 Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Ser Ser Arg Ser
39 1 5 10 15
40 Glu Ile Leu Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu
41 20 25 30
42 Asn Lys Lys Leu Glu Lys Ser Ser Thr Ser Thr Thr Ser Arg Val
43 35 40 45
44 Phe Ser Ser Lys Asp Lys Asp Pro Phe Ser Phe Thr Ser Thr Lys Thr

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45	50	55	60
46	Gln Leu Pro Asp Val Glu Ser Glu Thr Asp Ser Glu Gly Ser Asp Val		
47	65	70	75
48	Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp Phe Cys Asn		80
49	85	90	95
50	Leu Arg Gly Asn Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln		
51	100	105	110
52	Asp Asp Phe Asn Leu Cys Gly Leu Ser Gly Gln Val Pro Tyr Tyr Asp		
53	115	120	125
54	Tyr Ala Leu Asp Leu Ile Leu Asp Val Asp Ala Ser Asn Ser Glu Met		
55	130	135	140
56	Phe Thr Asp Glu Gln His Glu Met Val Glu Ser Ala Ala Glu Met Leu		
57	145	150	155
58	Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys Gly Met Ala		160
59	165	170	175
60	Ala Met Thr Glu Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg		
61	180	185	190
62	Val Phe Cys Cys Gly Gln Ser Cys Leu Pro Val Gly Gln Ser Asp Ile		
63	195	200	205
64	Pro Arg Ser Ser Thr Val Lys Ile Tyr Cys Pro Lys Cys Glu Asp Ile		
65	210	215	220
66	Ser Tyr Pro Arg Ser Lys Phe Gln Gly Asn Ile Asp Gly Ala Tyr Phe		
67	225	230	235
68	Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly Asn Leu Lys		240
69	245	250	255
70	Pro Gln Lys Pro Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys		
71	260	265	270
72	Val His Lys Pro		
73	275		

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/359,026

DATE: 12/15/1999
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Line ? Error/Warning

Original Text

32 W "N" or "Xaa" used: Feature required

cwndwsdskt sttcstt